

AMENDMENTS TO THE SPECIFICATION

Pursuant to 37 C.F.R. § 1.121(b)(1)(i), Applicants respectfully request that the Examiner make following amendments to the Specification.

(1) Applicants respectfully request that the Examiner replace the current Title of U.S. Patent Application Publication No. 2005/0226879 to Ulmann *et al.* with the Title listed below. Appendix A contains a marked-up version of replacement Title.

METHODS OF INHIBITING CELL CYCLE OF A CELL
COMPRISING ADMINISTERING A NUP153 INHIBITOR

(2) Applicants also respectfully request that the Examiner replace paragraphs [0006], [0012], [0017], and [0018] of U.S. Patent Application Publication No. 2005/0226879 A1 with the paragraphs listed below. Appendix A contains a marked-up version of replacement paragraphs [0006], [0012], [0017], and [0018].

[0006] FIG. 3 contains illustrations of the Nup153 nuclear pore protein determined to have a role in nuclear disassembly and a domain-specific recombinant protein containing the central zinc-finger region of Nup153. From top to bottom, the five sequences are represented by SEQ ID NOs: 36–40, respectively.

[0012] FIG. 9 shows the zinc finger domain of Nup153 associates with the COPI complex. FIG. 9A shows a silver staining of gel from GST pulldown assay. 2% of input (XEE, *Xenopus* egg extract) was loaded in lane 1. Molecular markers indicated are 198, 115, and 93 kD. (a) and (b) indicate two bands subjected to peptide sequencing. FIG. 9B shows sequences of peptides obtained from band (a) and band (b). Regarding band (a), from top to bottom, the sequences for ten peptides (SEQ ID NOs: 41, 43, 45, 47, 49, 51, 53, 55, 57, and 59) were aligned with those of homologous human proteins in the database (SEQ ID NOs: 42, 44, 46, 48, 50, 52, 54, 56, 58, and 60, respectively). Regarding band (b), from top to bottom, the sequences for six peptides (SEQ ID NOs: 61, 63, 65, 67, 69, 71, and 73) were aligned with those of homologous human proteins in the database (SEQ ID NOs: 62, 64, 66, 68, 70, and 72, respectively). FIG. 9C shows an immunoblot of GST pulldown samples with antibodies against human .alpha.-COP, .beta.-COP and .beta.'-COP, respectively.

[0017] FIG. 14 shows alignment of zinc fingers of human Nup153, Nup358, and Np14. The sequences for x153ZnF1–

x153ZnF4 are represented by SEQ ID NOs: 73-76, respectively; the sequences for h153Zn41-h153znF4 are represented by SEQ ID NOs: 77-80, respectively; the sequences for h358zF1-h358ZnF8 are represented by SEQ ID NOs: 81-88, respectively; the sequence for hNpl4 ZnF is represented by SEQ ID NO: 89; and the sequence for Consensus is represented by SEQ ID NO: 90.

[0018] FIG. 15 shows results of the phage display screen of Example 2. Peptides chosen for further testing are boxed. The two shades of text indicate sequences derived from two different wash conditions in the third round of selection. Basic residues (H, R, and K) are also highlighted. From top to bottom, these sixteen sequences are represented by SEQ ID NOs: 91-106, respectively.

Also, Applicants respectfully request that the Examiner amend the present Specification to include after the Listing of Claims and before the Drawings the attached amended "Sequence Listing". The amended "Sequence Listing" includes SEQ ID NOs: 36-106, which correspond to sequences found in FIGs. 3, 9, 14, and 15 as originally filed. The attached copy of the amended "Sequence Listing" is in "TXT" format, which is a Computer Readable Form. Therefore, the attached copy of the amended "Sequence Listing" complies with 37 C.F.R. § 1.821(e). As Applicants are filing the attached copy of the "Sequence Listing" as a "TXT" file via EFS-Web, Applicants submit that a statement under 37 C.F.R. § 1.821(f) is not required. Applicants also submit that the amended "Sequence Listing" does not include any new matter that goes beyond the disclosure of the application as filed.